SEQUENCE LISTING

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(ii) TITLE OF INVENTION: Sequence-Directed DNA Binding Molecules, Compositions and Methods

(iii) NUMBER OF SEQUENCES: 664

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(v) COMPUTER READABLE FORM:
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(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ferredoxin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTCTGCTTG CCAATGTCTT TATAGGTCAC CCGGAAGGCA CG 42

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human macrophage alpha1-antitrypsin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTACTGCCT CCACCCGAAG TCTACTTCCT GGGTGGGCAG GAAC 44

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene B for alpha 1-acid glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGTGACCGCC CATAGTTTAT TATAAAGGTG ACTGCACCCT GCAGCC 46

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for alpha 1 microtubulin-bikunin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATTGGAGCTG TCCTTGGGGC TGTAATTGGC CCCAGCTGAG CAGGGCA 47

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for alpha-2 macroglobulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTTTGCAC ACAGAGCAGC ATAAAGCCCA GTTGCTTTGG GAAGT 45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ACAA gene for peroxisomal 3-oxoacyl-CoA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTCGGGTTTG GCTACAAAAG GTGGAAAGAC TTCCGGTCTG CATTTCTG 48

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ACAA gene for peroxisomal 3-oxoacyl-CoA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAAGGTAGGC GGGGCATTGA GTGGAAAGCT CGGCTGGGCG GTGCCTGT 48

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human choline acetyltransferase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAATTGTGA CCCACAGCCT AATAATAACA GTCTTTGCCC TCTTGGCC 48

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human angiotensin I-converting enzyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCGGGGGTG TGTCGGGTTT TATAACCCGC AGGGCGGCCG CGGCG 45

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene fragment for the acetylcholine receptor gamma

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGTGGGAG TGTAGGCTGT TATATGACAC CCAGAGCCCA TCTCT 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytokine (Act-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTCCTAGGCC TCAGAGTCCC TATAAAGAGA GATTCCCAAC TCAGTA 46

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human beta-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGAGTGAG CGGCGCGGGG CCAATCGCGT GCGCCGTTCC GAAAG 45

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human beta-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGGCCGC GGCGGCGCCC TATAAAACCC AGCGGCGCGA CGCGCCA 47

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cardiac actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCCAACT GACCCTGTCC ATCAGCGTTC TATAAAGCGG CCCTCCTGGA 50

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for vascular smooth muscle alpha-actin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGAGAGCA GGCCAAGGGC TATATAACCC TTCAGCTTTC AGCTTCC 47

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human enteric smooth muscle gamma-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAGATCCGCC TCTGGGGTTT TATATTGCTC TGGTATTCAT GCCA 44

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human arachidonate 12-lipoxygenase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGGGGCCGC AGACCGGTCC TTTAAAGGTT GGAAGTGGCC CCGAGG 46

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alcohal dehydrogenase alpha subunit (ADH1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTGTTATTC AAGCAAAAAA AATAAATAAA TACCTATGCA ATACACCT 48

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alcohal dehydrogenase beta subunit gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGTTACAC AAGCAAACAA AATAAATATC TGTGCAATAT ATCTGCTT 48

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-fetoprotein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAACAGGCAT TGCCTGAAAA GAGTATAAAA GAATTTCAGC ATGATTTTCC 50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytosolic adenylate kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGCCGCGCG CTGACAGCCT TATAAATAGT CGCCTTTGCC GGCCGCC 47

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-N-acetylgalactosaminidase (AK1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGGACTTATC AGGTTACCGG ATTCGAGTCA GAAGCGGCGG CAGGTCTGAA 50

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ALAD gene for porphobilinogen synthase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATAAAGACCT TTGATCGGAT CTATCATTGT ACCTATCATA GGTCTG 46

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ALAD gene for porphobilinogen synthase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCCTACCAAG GAGGAAGACT GGATAAAATG GCCTGAGATG GCTGAA 46

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGAGTGACA AAGGCCTGAA TTTGTCAATT AGTAACAATT GTATTCAACA GTAAGGAT 58

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTGCTCACCA CACACAAGTG TTATAGGAGG AGTCTGGCCC TTGAG 45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase C gene for fructose 1,6-bisphosphate aldolase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACCTGCAATA CCCCCTTACC CCAATACCAA GACCAACTGG CATAG 45

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGCATAGAGC CAACTGAGAT AAATGCTATT TAAATAAAGT GTATTTAATG AATTTCTCCA 60

AGCTTACGGA 70

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCCACACG TCAACGATTC TATTTGAAGT TGGGCAGGGG GTGGC 45

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATTAGAGAAG ATCGGGGACA CATGTGGGGC TGGGCAGGAG CTG 43

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGGCTGGGCA GGAGCTGCCT TATAACCACC CGGGAACCCC TAGCT 45

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCGGAGGGCG GAGTGGTGCC TTTAAAAGGC CGGCGCCGCC TTCCGC. 46

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGCGCCGCCC CTTCCGAGGC TAAATCGCTT CCTCTCGGAA CGCGC 45

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAAAAACATG ATGAGAAGTC TATAAAAATT GTGTGCTACC AAAGA 45

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human leukemia inhibitory factor (LIF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTTACAACAC AGGCTCCAGT ATATAAATCA GGCAAATTCC CCATTTGAGC 50

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO
(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aminopeptidase N gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGGCTCCTC CCCTTTGGGG ATATAAGCCC GGCCTGGGGC TGCTCC 46

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAATGTGCTT CTTACAGGAA TATAAATAGT TTCTGGAAAG GACACTG 47

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human amyloid-beta protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGGAGGCCTG CGGGGTCGGA TGATTCAAGC TCACGGGGAC GAGCAGG 47

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human amyloid beta protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGGGACGAG CAGGAGCGCT CTCGACTTTT CTAGAGCCTC AGCGTCCTAG GACT 54

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human amyloid-beta protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCGGGGTGGG CCGGATCAGC TGACTCGCCT GGCTCTGAGC CCCGCCG 47

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human amyloid-beta protein (APP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCAGCTGACT CGCCTGGCTC TGAGCCCCGC CGCCGCGCTC GGGCTCCGTC 50

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pronatriodilatin precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGCTTGGAGA GCTGGGGGGC TATAAAAAGA GGCGGCACTG GGCAGC 46

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTGAAGTGGG AGCCTCTTGA GTCAAATCAG TAAGAATGCG GCTCTTGCA 49

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTGCGGATGA TAACTTTAAA AGGGCATCTC CTGCTGGCTT CTCACTTGG 49

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGCTTGGAGA GCTGGGGGGC TATAAAAAGA GGCGGCACTG GGCAGC 46

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human atrial natriuretic factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTTGGAGAGC TGGGGGGCTA TAAAAAGAGG CGGCACTGGG CAGCTGGGAG 50

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human angiotensinogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCCATCCCC ACCCCTCAGC TATAAATAGG GCCTCGTGAC CCGGCC 46

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human heart/skeletal muscle ATP/ADP translocator gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCGCGAGAGC CCGGCGGGGA TATAAGGGGG AGCTGCGGGC CAGGC 45

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TCTGGACACC CTGCCTCAGG CCCTCATCTC CACTGGTCAG CAGGTGACC 49

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTCAGGCCCT CATCTCCACT GGTCAGCAGG TGACCTTTGC CCAGCGCCC 49

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGCCTGCTGC CCTGGAGATG ATATAAAACA GGTCAGAACC CTCCTGCC 48

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GACACCCTGC CTCAGGCCCT CATCTCCACT GGTCAGCAGG TGACCTTTGC 50

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein CIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGCCTGCTGC CCTGGAGATG ATATAAAACA GGTCAGAACC CTCCTGCC 48

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein AII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATAATCCCTG CCCCACTGGG CCCATCCATA GTCCCTGTCA CCTGACAGG 49

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein AII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGGGTGGGTA AACAGACAGG TATATAGCCC CTTCCTCTCC AGCCAG 46

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fetal gene for apolipoprotein AI precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTGCAGACAT AAATAGGCCC TGCAAGAGCT GGC 33

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCCTGGGCTT CCTATAAATG GGGTGCGGGC GCCGGCCGC 39

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apoC-II gene for preproapolipoprotein C-II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGGAAGTGGG TCTCAACCAC TATAAATCCT CTCTGTGCCC GTCCGGA 47

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein C-I (VLDL) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGCCCCGCCC CTCCCCAGCC TGATAAAGGT CCTGCGGGCA GGACAGG 47

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein D gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCAGAGACC TGAAGAAGCT TATAAAATAG CTTGGGAGAG GCCAGTC 47

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human arginase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGTTGTTTAT TCAACCCAAG TATAAATGGA AAAAAAAGAT GCGCC 45

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human argininosuccinate synthetase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGCCCCCGG GCCCTGTGCT TATAACCTGG GATGGGCACC CCTGC 45

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human sodium/potassium ATPase alpha 3 subunit (ATP1 A3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCCCTCCCGC GGACGCGGGC ATATGAGGAG GCGGAGGCGG CGGC 44

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human (BSF-2/IL6) gene for B cell stimulatory factor-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATTAGAGTCT CAACCCCCAA TAAATATAGG ACTGGAGATG TCTGAGGC 48

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human C5 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTGAATTCT TCAAGTTCAG TTTATTTAAA AGGAGACTAT CCTCAAAAGT G 51

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CCTCCCCTTG TCGCCTAGGT CCACCCGAGC CCCCTCCCCC GGGCC 45

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACGAAGTT GGCGGGAGCC TATAAAAGCG GGCCGGCGCG ACCCGC 46

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human calcitonin/alpha-CGRP gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTCCCGACCC ACAGCGGCGG GAATAAGAGC AGTCGCTGGC GCTGG 45

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human calretinin gene, exon 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGGCGCAGG CTCCAGAGCG TATATAAGGG CAGCGTGGCG CACAACC 47

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cathepsin G gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TTCCTTCCTC TCTCAGGGCC TTAAAGTCTA GGAGGAGGAA GCACA 45

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase VII (CA VII) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTCCTCCCGC CAGCCGCTGC TTTAAGAGGC TGCTCCGCGG TAGCG 45

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cardiac beta myosin heavy chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCTAGTGACA ACAGCCCTTT CTAAATCCGG CTAGGGACTG GGTGCC 46

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cardiac beta myosin heavy chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TGGGGGTGCC TGCTGCCCCA TATATACAGC CCCTGAGACC AGGTC 45

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human complement C3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TGGGGGAAAG CAGGAGCCAG ATAAAAAGCC AGCTCCAGCA GGCGCTG 47

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human recognition/surface antigen

(CD4) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAGTCCTCA CACAGATACG CCTGTTTGAG AAGCAGCGGG CAAGAAAGAC 50

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hyaluronate receptor gene (CD44)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TAGGTCACTG TTTTCAACCT CGAATAAAAA CTGCAGCCAA CTTCCGAGGC 50

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane conductance reg. gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AATGACATCA CAGCAGGTCA GAGAAAAAGG GTTGAGCGGC AGGCACCCAG 50

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cholesterol 7-alpha-hydroxylase (CYP7) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATGGATCTGG ATACTATGTA TATAAAAAGC CTAGCTTGAG TCTCTT 46

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human choline acetyltransferase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGCAATTGTG ACCCACAGCC TAATAATAAC AGTCTTTGCC CTCTTGGCC 49

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human mast cell chymase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CTCTCTTGCC TTCTAGGAGT TATAAAACCC AAGACTGGAA AGGAAA 46

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human heart chymase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CCTCTCTTGC CTTCTGGGAG TTATAAAACC CAAGACTGGA AGGAAAA 47

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human creatine kinase B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGCCAATGGA ATGAATGGGC TATAAATAGC CGCCAATGGG CGGCCCGC 48

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human C-type natriuretic peptide gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACATCAGCGG CAGGTTGGAT TATAAAGGCG CGAGCAGAGT CACGGG 46

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTCCGCGCG GGGGTGGAGG GAGAGGAGGA GGTTCCTGCC GAGGT 45

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGGGCAAGG GCATCCTGAG GGGCGGGGCC GGGGGCGGAG CCTTGC 46

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATCCTGAGGG GCGGGGCCGG GGGCGGAGCC TTGCGGGCTG GAGCGA 46

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transmembrane protein (CD59) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGAGGGGCGG GGCCGGGGGC GGAGCCTTGC GGGCTGGAGC GAAAGAATGC 50

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human myeloid specific CD11b gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCCCTCTTCC TTTGAATCTC TGATAGACTT CTGCCTCCTA CTTCTC 46

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cholesteryl ester transferase protein (CETP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGGGGGCTG GGCGGACATA CATATACGGG CTCCAGGCTG AACGGC 46

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane conductance regulator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGGTGGGGG GAATTGGAAG CAAATGACAT CACAGCAGGT CAGAG 45

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cystic fibrosis transmembrane conductance regulator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTGGGGGGAA TTGGAAGCAA ATGACATCAC AGCAGGTCAG AGAAAAA 47

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human coseg gene for vasopressin-neurophysin precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CACGGGAACA CCTGCGGACA TAAATAGGCA GCCAGCAGAG GCAGCA 46

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human creatine kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TTCAGAGAAA GGGCAGGTGC TATAAAGGGC CCAGCGCCAC GGGCCT 46

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-B-crystallin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGAAGCTTCA CAAGACTGCA TATATAAGGG GCTGGCTGTA GCTGCAG 47

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human C3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTGGGGGAA AGCAGAGCCA GATAAAAAGC CAGCTCCAGC AGGCGCTGCT 50

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human colony stimulating factor
CSF-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCCTGGCCAG GGTGATTTCC CATAAACCAC ATGCCCCCCA GTCCTC 46

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytotoxic serine proteinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTTACTCAGC AGCAGGGGTG TAAATGTGAC AGTGCCATGT CAAC 44

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human CST3 gene for cystatin C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGCGGCGAAG GCCGGAAGGG ATAAAACCGC AGTCGCCGGC CTCGCG 46

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human CST4 gene for Cystatin D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TTGGGGGACA CCCAAGTAGG ATAAATGCAC AGCTAGCTTC TGGCC 45

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome P-450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ACTAAATTAG CAGGGAGTGT TATAAAAACT TTGGAGTGCA AGCTC 45

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cholesterol desmolase cytochrome gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AGCAGGAGGA AGGACGTGAA CATTTTATCA GCTTCTGGTA TGGCC 45

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cholesterol desmolase cytochrome P-450 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TATGGCCTTG AGCTGGTAGT TATAATCTTG GCCCTGGTGG CCCAGG 46

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human steriod 11-beta-hydroxylase (CYP11B1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAAGGCAAGG CACCAGGCAA GATAAAAGGA TTGCAGCTGA ACAGGGT 47

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human CYPXI gene for steroid 18-hydroxylase (P-450 C18)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CAGAGCAGGT TCCTGGGTGA GATAAAAGGA TTTGGGCTGA ACAGGGT 47

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human CYPXIX aromatase P-450 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TGGACAATAA ATGAAATCTC CATAAAAGGC CCAAAGGACA GGGTTC 46

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human decay-accelerating factor (DAF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AGCCCAGACC CCGCCCAAAG CACTCATTTA ACTGGTATTG CGGAGC 46

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human dopamine beta-hydroxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ACGTCCATGT GTCATTAGTG CCAATTAGAG GAGGGCAGCA GGCTG 45

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human dopamine beta-hydroxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ACCCCATTCA GGACCAGGGC ATAAATGGCC AGGTGGGACC AGAGAG 46

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human desmin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGGGCTGATG TCAGGAGGGA TACAAATAGT GCCGACGGCT GGGGGC 46

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytokeratin 8 (CK8) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CCCGGGGCTG GGATCTCTTT TATAAAAGGC CATTCCTGAG AGCTC 45

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human DNA polymerase alpha gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCCTCCCGAG CCGCTGATTG GCTTTCAGGC TGGCGCCTGT CTCGGCCCCC 50

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human dopamine D1A receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCTGTGCCCC GCGGGAACCC CGCCGGCCTG TGCGCTTGCT GGTGCCAGCT 50

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human eosinophil cationic protein (ECP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGACCCACCA AGGGAAGCTT TATTTAAACA GTTCCAAGTA GGGGAGA 47

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HER2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAGGAGGAGG GCTGCTTGAG GAAGTATAAG AATGAAGTTG TGAAGCTGAG 50

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human elastin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTGTCTCGCT GTGATAGATC AATAAATATT TTATTTTTTG TCCTGG 46

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human endothelial leukocyte adhesion molecule I (ELAM-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATTCACAGGA AGCAATCCCT CCTATAAAAG GGCCTCAGCC GAAGTAGTG 49

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human eosinophil major basic protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGAAGTTCCT CCAAGGCCTC TATATAAGAA GTCTTTGTGA GAGGAAG 47

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human preproenkephalin B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTCTAGGAAA GTTTCTCAGC TCTCAAACCT CTGTTTTCTC ATCTGCAAG 49

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human preproenkephalin B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TTCTCATCTG CAAGATGGGG ATAATATTAA CCAACTGGCT AGGTCATGAG 50

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ENO3 gene for muscle-specific enolase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGGGACCGAG TGGCTCAGGG ATAAATGCGC ACCTGAGAGG GGGTGA 46

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human eosinophil derived neurotoxin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CAACCCACCA AGGGATGCTT TATTTAAACA GTTCCAAGTA GGGGAGA 47

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human erythropoietin receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TACCCAGGCT GAGTGCTGGC CCCGCCCCCT CGGGGATCTG CCACTT 46

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human c-erb B2/neu protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

AGGAGGGCTG CTTGAGGAAG TATAAGAATG AAGTTGTGAA GCTGA 45

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ERCC2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CCGATTGGCT CTGCCCTAGC GGATTGACGG GCAGGTTAGC CAATGGTCT 49

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ERCC2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CAGGTTAGCC AATGGTCTCG TAATATAGGT GGAGCGAGCC CTCGAGG 47

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human erythropoietin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACCCGG CGCGCCCCAG GTCGCTGAGG GACCCCGGCC AGGCGCGGAG 50

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human oestrogen receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATATGAGCTC GGGAGACCAG TACTTAAAGT TGGAGGCCCG GGAGCCCA 48

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human elastase I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

AGCTTTGCTG CTAAGAGGAG TATAAAGAGG GCTTGGTCCA AGCAAG 46

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fibrinogen gamma chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCCCCGTGA TCAGCTCCAG CCATTTGCAG TCCTGGCTAT CCCA 44

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fibrinogen gamma chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGCTATCCC AGGAGCTTAC ATAAAGGGAC AATTGGAGCC TGAGA 45

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TTAACATCTC TAGTTCTCAC CCAATTCTCT TACCTGAGAA ATGGA 45

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GTTATCCGGG TGGCAAGCCC ATATTTAGGT CTATGAAAAT AGAAGCT 47

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lymphocyte IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AGCCCATATT TAGGTCTATG AAAATAGAAG CTGTCAGTGG CTCTAC 46

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apoferritin H gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGCCTGACG CCGACGCGGC TATAAGAGAC CACAAGCGAC CCGCA 45

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fibrinogen beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TATTAACTAA GGAAAGGTAA CCATTTCTGA AGTCATTCCT AGCAGA 46

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fibrinogen beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATTCCTAGCA GAGGACTCAG ATATATATAG GATTGAAGAT CTCTCAGTT 49

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human factor IX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CCAGAAGTAA ATACAGCTCA GCTTGTACTT TGGTACAACT AATCGACCTT 50

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human FK506 binding proteins 12A, 12B, and 12C (FKBP12)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAGCCGTGGA ACCGCCGCCA GGTCGCTGTT GGTCCACGCC GCCCGTCGCG 50

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human 5-lipoxygenase activating protein (FLAP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

TTGTGCCGGG GATCTTCAGA AATTGTAATG ATGAAAGAGT GCAAGCTCTC 50

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fos proto-oncogene (c-fos)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ATTCATAAAA CGCTTGTTAT AAAAGCAGTG GCTGCGGCGC CTCGTACTCC 50

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human GOS2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGCGTGTCTC AGAGAAAAGA TATAAGCGGC CCCCGGACGC TAAAG 45

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human granulocyte colony-stimulating factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CAGGCCTCCA TGGGGTTATG TATAAAGGGC CCCCTAGAGC TGGGCC 46

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human EGR2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CGGGTATTGA AGACCTGCCC ATAAATACTT AGAGCAACAC TTTCCGTC 48

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human growth hormone (hGH) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGGGAGAGAA GGGGCCAGGG TATAAAAAGG GCCCACAAGA GACCAG 46

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gastric inhibitory polypeptide (GIP) mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TAATCAGCAG GTCTATGCCT AATATAAAGG AGCTGGGGCA TGATTTCTTC 50

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human GLA gene for alpha-D-galactosidase A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAAACAATAA CGTCATTATT TAATAAGTCA TCGGTGATTG GTCCGC 46

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTTACAGATG AGAAATTTAT ATTGTCAGCG TAATATCTGT GAGG 44

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGCTAAACAG AGCTGGAGAG TATATAAAAG CAGTGCGCCT TGGTGCA 47

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human granulocyte-macrophage colony stimulating factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CATTAATCAT TTCCTCTGTG TATTTAAGAG CTCTTTTGCC AGTGAGC 47

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human glucocorticoid receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TGGGCAATGG GAGACTTTCT TAAATAGGGC TCTCCCCCCA CCCATG 46

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human growth hormone releasing factor (GRF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AACGCTTAGG AAAATGAAGA GATAAATGAT GGGAACGCCA GGCGGCTGCC 50

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human GST pi gene for glutathione S-transferase pi

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAGCGGGGCG GGACCACCCT TATAAGGCTC GGAGGCCGCG AGGC 44

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: human glycophorin C (GPC) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CAGAAGTGGG CGGGTGTGTG TTTAAAAAAA AAAAAAGGGG TGGAAAC 47

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone (H10) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CGCGGTCCGC CCGCCGCCGC TAAATACCCG GATGCGCCGC CCAAGC 46

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for H1 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTTGGAT TTGGGAATCT TATAAGTTCT GTATGAGACC ACTC 44

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human H1 histone gene FNC16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGCGGTGGAT TGGACGCTCC ACCAATCACA GGGCAGCGCC GGCTTA 46

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone gene FNC16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACCAATCACA GGGCAGCGCC GGCTTATATA AGCCCGGGCC CGAGCATAGC AGCA 54

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human H2B.2 and H2A.1 genes for
Histone H2A and H2B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

TTTTCGCGCC CAGCAGCTGC TATAAAATGC GCGTCCCTGT AGGTTCC 47

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human H4/a gene for H4 histone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGGGGCAGGG GTAACGTAGA TATATAAAGA TCGGTTTCCT ATTCTCTC 48

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human H4/b gene for H4 histone

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CTGCAAGTAT AGTGTGTGTG TATATATATA TATATACCTA GCAGTATTTA TTAAAT 56

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human androgen receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GGTGGGGGCG GGACCCGACT CGCAAACTGT TGCATTTGCT CTCCACCTCC 50

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin (hCG) beta subunit

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GCCCTCTCTC ATTGGGCAGA AGCTAAGTCC GAAGCCGCGC CCCTCCTGG 49

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human islet amyloid polypeptide (hIAPP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GCTGAGAAAG GTGTGAGGGG TATATAAGAG CTGGATTACT AGTTAGCAAA 50

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human H4 histone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTCCCGCCG GCGCGCTTTC GGTTTTCAAT CTGGTCCGAT ATCTCTGTAT AT 52

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human H4 histone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

AATCTGGTCC GATATCTCTG TATATTACGG GGAAGACGGT GACGCTC 47

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone H2a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TCCTCTTTTC TTGGCGAACT CAACTGGTAT GAATTCCTCA 40

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone H2a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CACAGCCTAC CTCCAGTCAG TATAAATACT TCTCTGCCTT GCGTTC 46

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone H2b gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

TATTTGCATA AGCGATTCTA TATAAAAGCG CCTTGTCATA CCCTGCT 47

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone H3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ATTTTTGAAT TTTCTTGGGT CCAATAGTTG GTGGTCTGAC TCTAT 45

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone H3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CAATAGTTGG TGGTCTGACT CTATAAAAGA AGAGTAGCTC TTTCCTT 47

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HLA-A1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

AGTGTCGTCG CGGTCGCTGT TCTAAAGTCC GCACGCACCC ACCGG 45

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HLA-B27 antigen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

AGTGTCGCCG GGGTCCCAGT TCTAAAGTCC CCACGCACCC ACCCGG 46

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HLA-Bw57 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

AGCGTCGCCG CGGTCCCAGT TCTAAAGTCC CCACGCACCC ACCCG 45

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HLA-F gene for human leukocyte antigen F

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TGTCGCCGCA GTTCCCAGGT TCTAAAGTCC CACGCACCCC GCGGGA 46

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for histocompatibility antigen HLA-A3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGTGTCGTCG CGGTCGCTGT TCTAAAGCCC GCACGCACCC ACCGGG 46

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for class I histocompatibility antigen HLA-CW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CATTGGGTGT CGGACCTCTA GAAGGCCGGT CAGCGTCTCC GC 42

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HMG-17 gene for non-histone chromosomal protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CGGTCCGGGG CTCCCAGCGC TATAAAAACT TTATAAACCC CCCGGA 46

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HOX3D gene for homeoprotein HOX3D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAGAAAGAGA TATCTCCACC TATAAATTGT CCACTTTGGA GAACAA 46

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human 71Kd heat shock cognate protein (hsc70)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

TGGAAGGTTC TAAGATAGGG TATAAGAGGC AGGGTGGCGG GCGGA 45

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human heat shock protein (hsp 70) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

AAGGCGGGTC TCCGTGACGA CTTATAAAAG CCCAGGGGCA AGCGGTCCGG 50

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CTTCGGTCTC ACGGACCGAT CCGCCCGAAC CTTCTCCCGG GGTCAG 46

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CCGCCCGGCT GACTCAGCCC GGGCGGGCGG GCGGGAGGCT CTCGAC 46

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CCGGCTGACT CAGCCCGGGC GGGCGGGCGG GAGGCTCTCG ACTGGG 46

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTGACTCAGC CCGGGCGGGC GGGCGGGAGG CTCTCGACTG GGCGGG 46

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGGCGGGCGG GAGGCTCTCG ACTGGGCGGG AAGGTGCGGG AAGGT 45

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hsp70B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CGGCGGGGTC GGGGAGGTGC AAAAGGATGA AAGCCCGTG GACGGAGCTG AGC 53

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human IAPP gene for islet amyloid polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GCTGAGAAAG GTGTGAGGGG TATATAAGAG CTGGATTACT AGTTAGC 47

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human intercellular adhesion molecule 1 (ICAM-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGGTTTCCGG GAAAGCAGCA CCGCCCCTTG GCCCCCAGGT GGCTAG 46

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human intercellular adhesion molecule 1 (ICAM-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GGCCCCCAGG TGGCTAGCGC TATAAAGGAT CACGCGCCCC AGTCGA 46

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon-inducible gene IFI-54K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

AAAGGAACCA GAGGCCACTG TATATATAGG TCTCTTCAGC ATTTATTG 48

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon alpha gene IFN-alpha 14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

ATGGAAGCTA GTATGTTCCT TATTTAAGAC CTATGCACAG AGCAAGGT 48

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon alpha gene IFN-alpha 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAAATTAGTA TGTTCACTAT TTAAGAACTA TGCACAGAGC AAAGT 45

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon alpha gene IFN-alpha 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATGGAAACTC GTATGTGACC TTTTTAAGAT CTGTGCACAA AACAAGGT 48

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon alpha gene IFN-alpha 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

ATGGAAACTA GTATGTTCCC TATTTAAGAC CTACACATAA AGCAAGGT 48

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon alpha gene IFN-alpha 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

ATGGAAATTA GTATGTTCAC TATTTAAGAC CTATGCACAG AGCAAAGT 48

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human immune interferon (INF-gamma) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TCCTCAGGAG ACTTCAATTA GGTATAAATA CCAGCAGCCA GAGGAGGTGC 50

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha/beta-interferon (IFN)-inducible 6-16 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GGGAGGATCC ACAAGTGATG ATAAAAAGCC AGCCTTCAGC CGGAG 45

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human insulin like growth factor II (IGF-2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTGGGAGGAG TCGGCTCACA CATAAAAGCT GAGGCACTGA CCAGCCT 47

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human insulin-like growth factor binding protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GTGGCGCGGC CTGTGCCCTT TATAAGGTGC GCGCTGTGTC CAGCG 45

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human germline leader peptide and variable region of 1154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CAACCTCCTG CACTGAAGCC TTATTAATAG GCTGGCCACA CTTCATGC 48

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human germline for leader peptide & variable region of 2908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CAACCTCCTG CCCTGAAGAC TTATTAATAG GCTGGACACA CTTCATGC 48

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human rearranged kappa immunoglobulin subgroup V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCACGACCAG GTGTTTGGAT TTTATAAACG GGCCGTTTGC ATTGTGAA 48

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human rearranged kappa immunoglobulin gene subgroup V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CGCCCTGCAG TCCAGAGCCC ATATCAATGC CTGGGTCAGA GCTCTGGA 48

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human germline fragment for immunoglobulin kappa light chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TGCCCTACCT TCCAGAGCCC ATATCAATGC CTGTGTCAGA GCCCTGGG 48

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human germline immunoglobulin kappa light chain V-segment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ACTTCCCTTG TGGGTCTGAG ATAAAAGCTC AGCTCTAACC CTTACC 46

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interleukin-2 (IL-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TATTTTTCCA GAATTAACAG TATAAATTGC ATCTCTTGTT CAAGAG 46

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for interleukin 1 alpha (IL-1 alpha)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CCACGCCTAC TTAAGACAAT TACAAAAGGC GAAGAAGACT GACTCAG 47

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for prointerleukin 1 beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TTGATTGTGA AATCAGGTAT TCAACAGAGA AATTTCTCAG CCTCCTAC 48

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for prointerleukin 1 beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTACTTCTGC TTTTGAAAGC TATAAAAACA GCGAGGGAGA AACTGGC 47

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: human interleukin 2 receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AGAAAGGATT CATAAATGAA GTTCAATCCT TCTCATCACC CCAGCCCA 48

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interleukin 2 receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TTTGAAAAAT TACCGCAAAC TATATTGTCA TCAAAAAAAA AAAAAA 46

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interleukin 4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ATCTGGTGTA ACGAAAATTT CCAATGTAAA CTCATTTTCC CTCGG 45

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interleukin 4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GGTTTCAGCA ATTTTAAATC TATATATAGA GATATCTTTG TCAGCATT 48

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human interleukin 5 (IL-5) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CATTTCCTCA AAGACAGACA ATAAATTGAC TGGGGACGCA GTCTTGTACT 50

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interleukin 7 (IL-7) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TTGCTTTGAT TCAGGCCAGC TGGTTTTTCT GCGGTGATTC GGAAATTCGC 50

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interleukin 9 gene (IL-9)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TTCCGTGTTT GAGAGGGAGC TTTAAATACC ACTCGATTTG AAGGTGTC 48

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human int-1 mammary oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACTTCAGCCA GCGCCGCAAC TATAAGAGGC GGTGCCGCCC GCCGT 45

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human jun-B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

TCCGTGGCTG ACTAGCGCGG TATAAAGGCG TGTGGCTCAG GCTGAG 46

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human DNA for 65 kD keratin type II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GCCCAACAAC CTCCTCAAAT GTATATAAAG GGATTTTTAT TGCACA 46

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ultra high-sulphur keratin protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TGGTGTGTTC CTATGTGGGA TATAAAGAGC CGGGGCTCAG GGGGCT 46

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-lactalbumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCTGAGGCTT TCTGCATGAA TATAAATAAA TGAAACTGAG TGATGCT 47

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human LAG-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GTCCTAGGCC TCAGAGTCCC TATAAGAGAG ATTCCCAACT CAGTA 45

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lecithin-cholesterol acyltransferase (LCAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

CTGAGGCTGT GCCCCTTTCC GGCAATCTCT GGCCACAACC CCCACTGG 48

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lecthin-cholesterol acyltransferase (LCAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

CCCCTCCCAC TCCCACACCA GATAAGGACA GCCCAGTGCC GCTTT 45

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lymphocyte-specific protein kinase (lck) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGGAGCAGAT CTTGGGGGAG CCCCTTCAGC CCCCTCTTCC ATTCCCTCAG 50

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human leukocyte fuction-associated antigen-1 (LFA-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGGTATCTCA CTGTGGTTTG ATTTGCATTT CTCTAATGAC TAATAGTG 48

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human leukocyte fuction-associated antigen-1 (LFA-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ATGTCTCTAA CTTGCTTACA CTTCCTCCCT GAACCCTGCG GTTTCA 46

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human leukocyte function-associated antigen-1 (LFA-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TCCTGCAGGC ACACCTCCCT CCCCGCCTGC CAGTGTCACC AGCCTGTT 48

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human leukocyte function-associated antigen-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CTGTTGCCTC TGTGAGAAAG TACCACTGTA AGAGGCCAAA GGGCATGATC 50

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: human lipoprotein lipase (LPL) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TATTTGCATA TTTCCAGTCA CATAAGCAGC CTTGGCGTGA AAACAGT 47

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human leukocyte adhesion molecule-1 (LAM-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TGGGTTAGAG AAATGAAAGA AGCAAGGCT TTCTGTTGAC ATTCAGTGCA 50

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lysozyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAAGGAAGT TAAAAGATGT TAAATACTGG GGCCAGCTCA CCCTGG 46

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human mannose binding protein 1 (MBP1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

AGGGATGGGT CATCTATTTC TATATAGCCT GCACCCAGAT TGTAGG 46

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human mast cell carboxypeptidase A (MC-CPA) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CATCAAGATA AGGGCTGAGG CATAAAACTG CCAGAGGGTC TCAAGG 46

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human P-glycoprotein (MDR1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CTTTGCCACA GGAAGCCTGA GCTCATTCGA GTAGCGGCTC TTCCA 45

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human bone marrow serine protease gene (medullasin)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

ACGGCCTCCC AGCACAGGGC TATAAGAGGA GCCGGGCGGG CACGG 45

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human microsomal epoxide hydrolase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TTGCTGTGCA GAGTCCAGGG GAGATAACCA CGCTGTGCAC ACATGAG 47

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human metallothionein-Ie gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GCAGCCAGTT GCAGGGCTCC ATTCTGCTTT CCAACTGCCT GACTGCTTGT TC 52

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human myoglobin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TTGTCAAGCA TCCCAGAAGG TATAAAAACG CCCTTGGGAC CAGGCA 46

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human melanoma growth stimulatory activity (MGSA) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GCTTTCCAGC CCCAACCATG CATAAAAGGG GTTCGCGGAT CTCGGAG 47

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-MHC gene for myosin heavy chain (N-terminus)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

AGAGGGTGGG GGAAACGGGA TATAAAGGAA CTGGAGCTTT GAGGAG 46

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human class II invariant gamma-chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GATTCCTCTC CAGCACCGAC TTTAAGAGGC GAGCCGGGGG GTCAG 45

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human motilin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CCCAGGGTTG GGAGGTATAT AAGAACCCGT CAGATCAGCC G 41

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human myeloperoxidase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CCACCCCCAG CTTAGAGGAC ATAAAAGCGC AGATTGAGCT AAGAGGAGCT 50

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human mitochondrial RNA-processing endoribonuclease RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

AAACACAATT TCTTTAGGGC TATAAAATAC TACTCTGTGA AGCTGAGGA 49

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human myc-oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAGGGAGGGA TCGCGCTGAG TATAAAAGCC GGTTTTCGGG GCTTTAT 47

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human Na,K-ATPase beta subunit (ATP1B) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GCACGGCCGC CGGGGCGCGG TATATAGTAA AGGTAGGGCG GGCGCA 46

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human neuromedin K receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAAGCGTGGG ACCCCATGAG TATAAAGAGA GCCTGTAGCG CAGG 44

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for heavy neurofiliment subunit (NF-H) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTGGACCCGG CCGCGGCGGC TATAAAAGGG CCGGCGCCCT GGTCGT 46

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human nuclear factor NF-IL6 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CGGTTGCTAC GGGCCGCCCT TATAAATAAC CGGGCTCAGG AGAAACT 47

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human neurofilament subunit NF-L gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGCGTCAGGA CCTCCCGGCG TATAAATAGG GGTGGCAGAA CGGCGC 46

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human neurokinin-2 receptor (NK-2) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TCTCTTCAGC GAAGGGGTTG ATTTATAAGG GTGTTTTCTG CTCTGACA 48

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human n-myc gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GGGTGTGTCA GATTTTTCAG TTAATAATAT CCCCCGAGCT TCAAAGCGC 49

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ornithine decarboxylase (ODC1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCATGGCGAC CCGCCGGTGC TATAAGTAGG GAGCGGCGTG CCGTGG 46

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ornithine transcarbamylase (OTC) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

ATACACAGCG GTGGAGCTTG GCATAAAGTT CAAATGCTCC TACACC 46

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human prepro-oxytocin-neurophysin I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTCCACCGAC GCAATGCCCA GGCATAAAAA GGCCAGGCCG AGAGACCGCC 50

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytochrome P450scc gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

TATGGCCTTG AGCTGGTAGT TATAATCTTG GCCCTGGTGG CCCAG 45

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human p53 gene for transmembrane related p53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CCCCTCCCAT GTGCTCAAGA CTGGCGCTAA AAGTTTTGAG CTTCTCAAAA 50

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GGGAGGCCTG CGGGGTCGGA TGATTCAAGC TCACGGGGAC GAGCAGG 47

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

CGGGGACGAG CAGGAGCGCT CTCGACTTTT CTAGAGCCTC AGCGTCCTAG GACT 54

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GCGGGGTGGG CCGGATCAGC TGACTCGCCT GGCTCTGAGC CCCGCCGC 48

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human Alzheimer's disease amyloid A4 precursor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CCGCCGCCGC GCTCGGGCTC CGTCAGTTTC CTCGGCAGCG GTAGGCGAG 49

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for plasminogen activator inhibitor 1 (PAI-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TATTTCCTGC CCACATCTGG TATAAAAGGA GGCAGTGGCC CACAGAG 47

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human platelet-derived growth factor A-chain (PDGF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

AGGGGCGCGG CGGCGGCGGC TATAACCCTC TCCCCGCCGC CGGCC 45

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human PGP9.5 gene for neuron-specific ubiquitin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ACAGTGCGTC TGGCCGGCGC TTTATAGCTG CAGCCTGGCG CTCCGC 46

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human plasminogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

CTCCACCGAC GCAATGCCCA GGCATAAAAA GGCCAGGCCG AGAGACCGCC 50

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human phenylethanolamine N-methylase (PNMT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TCGGGGCGGG GGTCGGGCGG TAGAAAAAAG GGCCGCGAGG CGAGCGGGG 49

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human opiomelanocortin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CTCCCCGTGT GCAGACGGTG ATATTTACCG CCAAATGCGA ACCAGGC 47

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene PRB3L for proline-rich protein G1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCCACTGTTC TGCTCCTCTT TATAAAGGGA GCTGCCATGG TTCTCC 46

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human PRB4 gene for proline-rich protein Po

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

CATTGTTTTG CTCCTCTTTA TAAAGGGAGT TGCCACGTTC CTCC 44

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human prolactin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

AGGCTTTGAT ATCAAAGGTT TATAAAGCCA ATATCTGGGA AAGAGA 46

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human prothymosin-alpha gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

CCGAGCGCCG CCCACTAATC TATATTAAAG CTTCTGGCGC CGCGTG 46

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human protamine 2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TCATAGTGGG CGTCCCCCTT TATATACAAG CTCCCGGGGA GCCTTG 46

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human SPR2-1 gene for small proline rich protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTGGGTGGGG TAGCAGGCTC TATAAAGAGA TCCTCTGCTG CACGAC 46

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human estrogen-responsive gene pS2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TAAGCAAACA GAGCCTGCCC TATAAAATCC GGGGCTCGGG CGGCCTC 47

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pulmonary surfactant apoprotein (PSAP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AGCCTGGCAG CCCCCACATC TATAAATGCT GCGTCTACCT TACCCT 46

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for prostatic secretory protein PSP-94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TGCGTGGTTG CCCTCTCCAG TATAAAAGTT TGATGCAGCT TTTCC 45

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human parathyroid hormone-related peptide (PTHRP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GAGGTAGACA GACAGCTATG TATATATATG TGGGTTTCGC TACAAGTGG 49

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for purine nucleoside phosphorylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

CTGGGGACTC CAGGGCAAGG GATATAAGCC AGAGCCTAGA CCAGTG 46

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human rDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

ATTTTGGGCC GCCGGGTTAT 20

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human regenerating protein (reg) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GTTCTTATCT CAGATCCTGA TATAAAGCTC CTACAGCTAC CTGGCC 46

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human renin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATCACCCCAT GCATGGAGTG TATAAAAGGG GAAGGGCTAA GGGAGCC 47

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene fragment for retinol binding protein (RBP)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

CGACCCCCTC CCCCCGGCGC TATAAAGCAG CGGGGCGGCC GCGGCG 46

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human serum amyloid A (GSAA1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

CACCCCGCTA ATTTAAAAAA TATATATACA GATATATAGT GGAGATGG 48

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human SAA1 beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

AACCAGCAGG GAAGGCTCAG TATAAATAGC AGCCACCGCT CCCTGGC 47

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human gene fragment for HLA class II SB 4-beta chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

CTACTTGGGT TCATGGTCTC TAATATTTCA AACAGGAGCT CCCTTTAG 48

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human c-sis proto-oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TCGCACTCTC CCTTCTCCTT TATAAAGGCC GGAACAGCTG AAAGGG 46

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human SLPI gene for secretory leukocyte protease inhibitor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

CACACCCACT GGTGAAAGAA TAAATAGTGA GGTTTGGCAT TGGCCA 46

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human superoxide dismutase (SOD-1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

CGAGGCGCGG AGGTCTGGCC TATAAAGTAG TCGCGGAGAC GGGGTG 46

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ornithine decarboxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

TCCATGGCGA CCCGCCGGTG CTATAAGTAG GGAGCGGCGT GCCGT 45

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human steroid 5-alpha-reductase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CTGCCCCCGC GCCGCCGCCC TATATGTTGC CCGCCGCGGC CTCTG 45

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human substance P receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GTGACGTCTC TGCAGGGGGT TATAAAAGCC TCGTGCGCAG CTAA 44

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human synaptobrevin 1 (SYB1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CCGGGAGGCG TGGTCAGCAC TAATAAAGGC GGAGGCCGGC GCGGCA 46

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human tyrosine aminotransferase
(TAT) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

CAACGCCCAT TTGTGGAGAC TATTTCAGGA GTTAGGATTT GCATCTG 47

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GACAGATGCA TTCTGTGGGG ATAAAATGTC ACAAAATTCA TTTCTTT 47

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

TCACAGAGGG CCTGGTCTAG AATATTCCAC ATCTGCTCTC ACTCT 45

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GACAGATGCA TTCTGTGGGG ATAAAATGTC ACAAAATTCA TTTCTTT 47

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

TCACAGAGGG CCTGGTCTGG AATATTCCAC ATCTGCTCTC ACTCTG 46

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human T-cell receptor V-beta chain gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

TGTTACTGTA GGAACTACCG TATAAGGACA GGATGTCCCA CCTCC 45

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transferrin (Tf) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

CCGCCCAGGC CGGGAATGGA ATAAAGGGAC GCGGGGCGCC GGAGG 45

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interleukin 3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GGGCACCTTG 10

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human tissue factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

CGGGAGAGCG CGCCGCCGGC CCTTTATAGC GCGCGGGGCA CCGGCTCCCC 50

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transforming growth factor-beta (TGF-beta)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

TGCCTTGCCC ATGGGGGCTG TATTTAAGGA CACCGTGCCC CAAGCCC 47

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transforming growth factor beta-3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAGACGTCAT GGGAGGGAGG TATAAAATTT CAGCAGAGAG AAATAGA 47

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transforming growth factor beta-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

CACGTGGTTC AGAGAGAACT TATAAATCTC CCCTCCCCGC GAAGA 45

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human tyrosine hydroxylase (TH) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GGCTTTGACG TCAGCTCAGC TTATAAGAGG CTGCTGGGCC AGGGCT 46

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human metallothionein gene IIA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

TCGTCCCGGC TCTTTCTAGC TATAAACACT GCTTGCCGCG CTGCAC 46

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human thrombospondin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

CCCAGGAATG CGAGCGCCCC TTTAAAAGCG CGCGGCTCCT CCGCCT 46

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human thyroxine-binding globulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ATAATGTTGC TATAACATCT GAATGACAGT CCATGGCATT ATTTC 45

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human thyroglobulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAAAGTGCCA ACGGCAGCTC TATAAAAGCT CCCTGGCCAG GGGACCT 47

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for tumor necrosis factor (TNF-alpha)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

CTCCTCTCGC CCCAGGGACA TATAAAGGCA GTTGTTGGCA CACCCA 46

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human lymphotoxin (TNF-beta) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GCTGCCACTG CCGCTTCCTC TATAAAGGGA CCTGAGCGTC CGGGCC 46

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human type I DNA topoisomerase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

TGACGTCGCC GACGTGTTGT TTAAAAGCGG CCGCGCAGGC GCAGTGAGCC 50

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human triosephosphate isomerase (TPI) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AGTTCCACTT CGCGGCGCTC TATATAAGTG GGCAGTGGCC GGACTGC 47

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human thyroid peroxidase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

ATCCAAGCGC AGAGTCAGTT TATAAGGTGG GTAACCAAGT CCCT 44

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transferrin receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GGCCGGGGGC GGGGCCAGGC TATAAACCGC CGGTTAGGGG CCGCCA 46

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human tryptase -I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

CGCCCCCTCC TGATCTGGAA GGATAAATGG GGAGGGGAGA GCCACTGGGT 50

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human beta 2 gene for beta-tubulin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

GCGGAGGCGG GCAGGGAGGG TATATAAGCG TTGGCGGACG GTCGGT 46

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for U 6 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GTATTTCGAT TTCTTGGCTT TATATATCTT GTGGAAAGGA CGAAAC 46

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human uPA gene for urokinase-plasminogen activator

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GGCGGCGCCG GGGCGGGCCC TGATATAGAG CAGGCGCCGC GGGTCGC 47

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human proto-oncogene vav

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GCAGGCGTGC GGGCGGGTGG GTGGTGGAGG CTGCGA 36

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human vascular cell adhesion molecule-1 (VCAM1) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GCCTCTGCAA CAAGACCCTT TATAAAGCAC AGACTTTCTA TTTCA 45

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human vimentin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ACCCTCTTTC CTAACGGGGT TATAAAAACA GCGCCCTCGG CGGGG 45

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human U1 RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GTAAAGGGTG AGGTATATGG AGCTGTGACA GGGCAGAAGT GTGTGAAGTC 50

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for small nuclear U1 RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GTAAAGAGTG AGGCGTATGA GGCTGTGTCG GGGCAGAGGC CCAAGATCTC 50

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human small nuclear U2 RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

TTGAATGTGG ATGAGAGTGG GACGGTGACG GCGGGCGCGA AGGCGAGCGC 50

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human U3 small nuclear RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

AAAAGTTTGC GGCAGATGTA GACCTAGCAG AGGTGTGCGA GGAGGCCGTT 50

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human U4C small nuclear RNA gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

AAATGGTAGT CATCATCCGT GGGGGAGCGG GGCGCGAATA AAGCCTTTCC 50

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone H3.3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GGGCGGGGCG GCGTGTGTTG GGGGATAGCC TCGGTGTCAG CCATCTTTCA 50

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human histone H4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

AGTTCGGTCC GCCAACTGTC GTATAAAGGC GCTGCCTCAG GTCAGAGGCC 50

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human non-histone chromosomal protein HMG-14 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

TGGGGGGCGG CCCGGCCGGC GGGGAGGGGG AGCCGCGGCC GGGACGCGGG 50

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ribosomal protein S14 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

AAGTAATAAA CCGTCTTTCC TTATGACGAG TCTTAAACTC TTTGGGAGGA 50

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for alpha tubulin (b alpha 1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

CGCGACCGAG GGTCTGGGCG TCCCGGCTGG GCCCCGTGTC TGTGCGCACG 50

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human skeletal alpha-actin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

AGGGAATCGC CCGCGGGCTA TATAAAACCT GAGCAGAGGG ACAAGCGGCC 50

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human epidermal 67-kDa Keratin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GGAAGATCTT GTGTGATAAA ACAATTACCA CATGAACCAA TCTTGCATGC 50

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human 50 KDatype I epidermal keratin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GACCCGCCCC CTACCCATGA GTATAAAGCA CTCGCATCCC TTTGCAATTT 50

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-1 collagen type I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

CTGCTCTCCA TCAGGACAGT ATAAAAGGGG CCCGGGCCAG TCGTCGGAGC 50

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human collagen type-III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GTGAGGGAAG CCAAACTTTT TCCTATTTAA GGCCAAAGCA AAGGAATCTC 50

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pro-alpha-2 (I) mRNA for
collagen N-prepropeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

CAGGGAAACT TTTGCCGTAT AAATAGGGCA GATCCGGGAT TTGTTATTTT 50

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human fibronectin (FN) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

TCCAGAGGGG CGGGAGGGCC GTCCCATATA AGCCCGGCTC CCGCGCTCCG 50

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human von Willebrand factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

TGTTTCCTTT TGGTAATTAA AAGGAGGCCA ATCCCCTGTT GTGGCAGCTC 50

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for fibrinogen gamma chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TGGCTATCCC AGGAGCTTAC ATAAAGGGAC AATTGGAGCC TGAGA 45

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for fibrinogen gamma chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

CAGTCCTGGC TATCCCAGGA GCTTACATAA AGGGACAATT GGAGCCTGAG 50

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human involucrin mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

AGGCCAGGCT GCAGAATGAT ATAAAGAGTG CCCTGACTCC TGCTCAGCTC 50

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein A-I and C-III genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

CCAGACCCTG GCTGCAGACA TAAATAGGCC CTGCAAGAGC TGGCTGCTTA 50

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein B-100 (apoB) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GCTCTTGCAG CCTGGGCTTC CTATAAATGG GGTGCGGGCG CCGGCCGCGC 50

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human apolipoprotein A-I and C-III genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

TCTAGGGATG AACTGAGCAG 20

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Humanapolipoprotein A-I and C-III genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

ACAGGCAGGA GGGTTCTGAC CTGTTTTATA TCATCTCCAG GGCAGCAGGC A 51

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

TACAATTATT GGTTAAAGAA GTATATTAGT GCTAATTTCC CTCCGTTTGT 50

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human albumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

TACAATTATT GGTTAAAGAA GTATATTAGT GCTAATTTCC CTCCGTTTGT C 51

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human serum prealbumin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

CCTAGCTCAG GAGAAGTGAG TATAAAAGCC CCAGGCTGGG AGCAGCCATC 50

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-fetoprotein (AFP) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

TAACAGGCAT TGCCTGAAAA GAGTATAAAA GAATTTCAGC ATGATTTTCC 50

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human C-reactive protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

AGGCAGGAGG AGGTAGCTCT AAGGCAAGAG ATCTGGGACT T 41

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene A for alpha 1-acid glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

AAGTGACCGC CCATAGTTTA TTATAAAGGT GACTGCACCC TGCAGCCACC 50

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene A for alpha 1-acid glycoprotein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

AAGTGACCGC CCATAGTTTA TTATAAAGGT GACTGCACCC TGCAGCCACC A 51

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for L apoferritin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

CGGCGCACCA TAAAAGAAGC CGCCCTAGCC ACGTCCCCTC 40

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for L apoferritin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

CGGCGCACCA TAAAAGAAGC CGCCCTAGCC ACGTCCCCTC G 41

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Olive baboon alpha-1 globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

GGCGTGCCCC CGCGCCCGGA GCATAAACCC TGGCGCGCTC GCGGCCCGGC 50

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Olive baboon alpha-1 globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GGCGTGCCCC CGCGCCCGGA GCATAAACCC TGGCGCGCTC GCGGCCCGGC A 51

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-globin germ line gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GTGCCAACAA TGGAGGTGTT TACCTGTCTC AGACCAAGGA CCTCTCTGCA 50

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Chimpanzee gene for alpha-like zeta-1-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

CCTGGCTGGG CCCAGCTCCC TGTATATAAG GGGACCCTGG GGGCTGAGCA 50

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Chimpanzee gene for alpha-like zeta-1-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

CCTGGCTGGG CCCAGCTCCC TGTATATAAG GGGACCCTGG GGGCTGAGCA C 51

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha globin gene cluster on chromosome 16: zeta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

CTGGCTGGGC CCAGCTCCCT GTATATAAGG GGACCCTGGG GGCTGAGCAC 50

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human theta 1-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

CCGCGGGACC CCTGGCCGGT CCGCGCAGGC GCAGCGGGGT CGCAGGGCGC 50

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Macaque cynomolgus beta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GCAGGAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT 50

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Chimpanzee beta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GCAGAAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT 50

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human germ line gene for beta-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GCAGGAGCCA GGGCTGGGCA TAAAAGTCAG GGCAGAGCCA TCTATTGCTT 50

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Spider monkey (A.geoffroyi) delta-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

CAGGGAGAAC AGGACCAGCA TAAAAGGCAG GGCAGGGCTA ACTGTTGCTT 50

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human transferrin receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GGGCGGGGCC AGGCTATAAA CCGCCGGTTA GGGGCCGCCA TCCCCTCAGA 50

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human beta-2-adrenergic receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

AGTTCCCCTA AAGTCCTGTG CACATAACGG GCAGAACGCA CTGCGAAGCG 50

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human IgE receptor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GGTGGCAAGC CCATATTTAG GTCTATGAAA ATAGAAGCTG TCAGTGGCTC 50

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human oncogene c-fos

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

TTCATAAAAC GCTTGTTATA AAAGCAGTGG CTGCGGCGCC TCGTACTCCA 50

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human c-myc oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

AATCTCCGCC CACCGGCCCT TTATAATGCG AGGGTCTGGA CGGCTGAGGA 50

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

CCGCCCCTCC GCGCCGCCTG CCCGCCCGCC CGCCGCGCTC CCGCCCGCCG 50

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human p53 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

ACTCCATTTC CTTTGCTTCC TCCGGCAGGC GGATTACTTG CCCTTACTTG 50

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene homologous to bladder carcinoma oncogene T24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

CGCGGCCCTA CTGGCTCCGC CTCCCGCGTT GCTCCCGGAA GCCCCGCCCG 50

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human c-abl gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GGGGCGGGCC TGGCGGGCGC CCTCTCCGGG CCCTTTGTTA ACAGGCGCGT 50

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human metallothionein-i-a gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

CGGCCCTCTT TCCCCTGACC ATAAAAGCAG CCGCTGGCTG CTGGGCCCTA 50

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human metallothinonein I-B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ACCCCACCAC CTCCCCCGAC TATAAAGGAG CAGCCAGCTC CTGGGCTCCA 50

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human metallothionein-If (MT-IF) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

CCCGGCCCCC TCCCCTGACT ATCAAAGCAG CGGCCGGCTG TTTGGGTCCA 50

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for 27 Kda heat shock protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

CCCTCAAACG GGTCATTGCC ATTAATAGAG ACCTCAAACA CCGCCTGCTA 50

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human 70 kDa heat shock protein gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GCGGGTCTCC GTGACGACTT ATAAAACCCC AGGGGCAAGC GGTCCGGATA 50

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human macrophage alpha1-antitrypsin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

TGCCTCCACC CGAAGTCTAC TTCCTGGGTG GGCAGGAACT GGGCACTGTG 50

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alphal-antitrypsin (S variant) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

CGTTGCCCCT CTGGATCCAC TGCTTAAATA CGGACGAGGA CAGGGCCCTG 50

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human S variable segment 5'of antithrombin III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

TCTGCCCCAC CCTGTCCTCT GGAACCTCTG CGAGATTTAG AGGAAAGAAC 50

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pulmonary surfactant protein (SP5) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

CCCCTCTCCC TACGGACACA TATAAGACCC TGGTCACACC TGGGAGAGGA 50

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human Immunoglobulin kappa L-chain V region gene (HK122)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

CCCCCTGCCC TGAAGACTTT TTATAGGCTG GTCACACCCG GAGCAGGAGT 50

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T cell receptor V-alpha/J-alpha chain (rearranged)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TTAAGGTTTG AATCCTCAGT GAACCAGGGC AGAAAAGAAT GATGAAATCC 50

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for HLA-DR alpha heavy chain (class II antigen)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

TGCATTTTAA TGGTCAGACT CTATTACACC CCACATTCTC TTTTCTTTTA 50

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human MHC class IIHLA-DC-3-beta gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

CTACCACGCA TGGAAACATC CACAGATTTT TATTCTTTCT GCCAGGTACA 50

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell receptor CD3-gamma gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GCCTTCTCTC AAAGGCCCCA GCCCCAACAG TGATGGGTGG AGCCAGTCTA 50

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pregnancy-specific beta-1 glycoprotein mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

CTGCCCTGGG AAGAGGCTCA GCACAGAAAG AGGAAGGACA GCACAGCTGA 50

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pregnancy-specific beta-1-glycoprotein 5 (PSG5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

AGAGAGGAGG GGACAGAGAG GTGTCCTGGG CCTGACCCCA CCCATGAGCC 50

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human factor VIII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

CCTGTGGCTG CTTCCCACTG ATAAAAAGGA AGCAATCCTA TCGGTTACTG 50

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ubiquitin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

TGACGCAACA CTCGTTGCAT AAATTTGCCT CCGCCAGCCC GGAGCATTTA 50

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human proliferating cell nucleolar protein P120 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

ACTATAATAC GCCAAGCGTG CGTTCTGCCG TTCCCTCCGA CACGCGCGAC 50

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for delta-globin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

CAGGGAGGAC AGGACCAGCA TAAAAGGCAG GGCAGAGTCG ACTGTTGCTT 50

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Gorilla fetal A-gamma-globin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTCCA GCAGTTCCAC 50

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for fetal A-gamma and G-gamma hemoglobin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTTCA GCAGTTCCAC 50

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Orangutan epsilon-globin gene with flanking Alu repeats

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

CAGAACTTCG GCAGTGAAGA ATAAAAGGCC ACACAGAGAG GCAGCAGCAC 50

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human haptoglobin (Hpl) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

TAAAAAGACC AGCAGATGCC CCACAGCACT GCTCTTCCAG AGGCAAGACC 50

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human low molecular weight oligoadenylate synthetase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

AAGACAGCTC CTCCCTTCTG AGGAAACGAA ACCAACAGCA GTCCAAGCTC AGTCAGCAGA 60

AGAGATAAAA G 71

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene fragment for dihydrofolate reductase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GGGGGGCGGG GCCTCGCCTG CACAAATAGG GACGAGGGGG CGGGGCGGCC 50

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human thymidine kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GGCTCGTGAT TGGCCAGCAC GCCGTGGTTT AAAGCGGTCG GCGCGGGACC 50

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human adenosine deaminase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCGGGAGGCG GGGCCCGGCC CGTTAAGAAG AGCGTGGCCG GCCGCGGCC 49

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human argininosuccinate synthase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TGCCCCCGGG CCCTGTGCTT ATAACCTGGG ATGGGCACCC CTGCCAGTCC 50

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ornithine aminotransferase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGGGGCGGGG CAGAATCAGC CTTTAAGTTG CAGTGACGCT CCGGCGTCAC 50

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human tyrosine hydroxylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

TGACGTCAGC TCAGCTTATA AGAGGCTGCT GGGCCAGGGC TGTGG 45

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human HMG CoA reductase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

CAGCTCCGAG CGTGCGTAAG GTGAGGGCTC CTTCCGCTCC GCGACTGCGT 50

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for lecithin-cholesterol acyltransferase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CCTAGGGCCC CTCCCACTCC CACACCAGAT AAGGACAGCC CAGTGCCGCT 50

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human porphobilinogen deaminase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

CGCCCAGAGG GAGGGACCTC CCCTTCGAGG GAGGGCGCCG GAAGTGACGC 50

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human porphobilinogen deaminasegene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GCACAGCACT CCCACTGACA ACTGCCTTGG TCAAGGTGGG CTTCAGGGCT 50

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human URO-D gene for uroporphyrinogen decarboxylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GGGGGGCAGG CTCAGATTCA GGTTAAATTG TGGATTGAGC TCGCAGTTAC 50

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human URO-D gene for uroporphyrinogen decarboxylase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GGGGGGCAGG CTCAGATTCA GGTTAAATTG TGGATTGAGC TCGCAGTTAC A 51

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase B (ALDOB) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

AAAAAAAAAA CATGATGAGA AGTCTATAAA AATTGTGTGC TACCAAAGAT 50

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GGTGGCGCTG CTCACCACAC ACAAGTGTTA TAGGAGGAGT CTGGCCCTTG 50

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GGTGGCGCTG CTCACCACAC ACAAGTGTTA TAGGAGGAGT CTGGCCCTTG A 51

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

TGTGGGGCGG GCAGGAGCTG CCTTATAACC AGCCCGGGAA CCCCTAGCTC 50

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

TGTGGGGCGG GCAGGAGCTG CCTTATAACC AGCCCGGGAA CCCCTAGCTC A 51

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GCTCGGCGGA GGGCGGAGTG GTGCCTTTAA AAGGCCGGGC GCCGCCTTCC 50

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GCTCGGCGGA GGGCGGAGTG GTGCCTTTAA AAGGCCGGGC GCCGCCTTCC G 51

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GCTAAATCGG CTGCGTTCCT CTCGGAACGC GCCGCAGAAG GGGTCCTGGT 50

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human aldolase A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GCTAAATCGG CTGCGTTCCT CTCGGAACGC GCCGCAGAAG GGGTCCTGGT G 51

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human phosphoglycerate kinase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GAGGCGGGGT GTGGGGCGGT AGTGTGGGCC CTGTTCCTGC CCGCGCGGTG 50

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for glucose 6-phosphate dehydrogenase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

CAGGCGCCCG CCCCCGCCCC CGCCGATTAA ATGGGCCGGC GGGGCTCAGC 50

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hepatic lipase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GCAGTCTTCC CTAACAAAGT ATCTAATAGG CATTGTGGTC TCTTTGGCTT 50

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human hepatic lipase mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GCAGTCTTCC CTAACAAAGT ATCTAATAGG CATTGTGGTC TCTTTGGCTT C 51

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human protein C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

AGTGCTGAGG GCCAAGCAAA TATTTGTGGT TATGGATTAA CTCGAACTCC 50

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human factor IX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

CCAGAAGTAA ATACAGCTCA GCTTGTACTT TGGTACAACT AATCGACCTT 50

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human MHC III HLA factor B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GCAGGTGCCA GAACACAGAT TGTATAAAAG GCTGGGGGCT GGTGGGGAGC 50

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pepsinogen gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

CGATAAGGCG GGACCCAACT TGTATATAAG GGCAGCTCAT GCTGCTGCTC 50

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pepsinogen C gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

CGATTAGACT AATCTTGGGC GTATAAAAGA GGAAAGAGTG CCCAGGTCTT 50

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human collagenase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

CTGGAAGGGC AAGGACTCTA TATATACAGA GGGAGCTTCC TAGCTGGGAT 50

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human stromelysin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

CCAAACAAAC ACTGTCACTC TTTAAAAGCT GCGCTCCCGA GGTTGGACCT 50

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

TCTGATCCGT GCAGGGTATT AATGTGTCAG GGCTGAGTGT TCTGAGATTT 50

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pancreatic alpha-amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

TGTAAAATGT GCTTCTTACA GGAATATAAA TAGTTTCTGG AAAGGACACT 50

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human pancreatic amylase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

TGTAAAATGT GCTTCTTACA GGAATATAAA TAGTTTCTGG AAAGGACACT 50

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: human cytochrome P450c gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GCCACACGTA CAAGCCCGCC TATAAAGGTG GCAGTGCCTT CACCCTCACC 50

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytochrome P-450c gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GCCACACGTA CAAGCCCGCC TATAAAGGTG GCAGTGCCTT CACCCTCACC C 51

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for cytochrome P(1)-450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

CACGTACAAG CCCGCCTATA AAGGTGGCAG TGCCTTCACC 40

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human steroid 21-hydroxylase [P450 (C21)] B gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GGATGGCTGG GGCTCTTGAG CTATAAGTGG CACCTCAGGG CCCTGACGGG 50

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human mitochonrial aldehyde dehydrogenase 2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

TTCCTGACCA TGGTACTTAT AAAAGCAGTG CCGTCTGCCC CATCCATGTC 50

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human carbonic anhydrase III gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

AAGGCCATGC AAGTGTGCGG GGGAGCTACA TAAAAGCGCG GGCTCGCGCG 50

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human creatine kinase B isozyme gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

TGGGCGGCCC GCGTTGTGCC CCTTAAGAGC CGCGGGAGCG CGGAGCGGCC 50

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human preproenkephalin A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

CTTCGGTTTG GGGCTAATTA TAAAGTGGCT CCAGCAGCCG TTAAGCCCCG 50

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human preprokephalin A gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

CTTCGGTTTG GGGCTAATTA TAAAGTGGCT CCAGCAGCCG TTAAGCCCCG G 51

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human prepro form of corticotropin releasing factor gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

TTTTTGAAGA GGGTCGACAC TATAAAATCC CACTCCAGGC TCTGGAGTGG 50

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human preprothyrotropin-releasing hormone gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GACCTCACTC GAGCCGCCGC CTGGCGCAGA TATAAGCGGC GGCCCATCTG 50

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for fetal A-gamma and G-gamma hemoglobin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CGGCTGGCTA GGGATGAAGA ATAAAAGGAA GCACCCTTCA GCAGTTCCAC 50

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene coding for ACTH and beta-LPH precursors

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

CCCACCAGGA GAGCTCGGCA AGTATATAAG GACAGAGGAG CGCGGGACCA 50

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human somatostatin I gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

TAGCCTGACG TCAGAGAGAG AGTTTAAAAC AGAGGGAGAC GGTTGAGAGC 50

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GTGAGGCTAA ACAGAGCTGG AGAGTATATA AAAGCAGTGC GCCTTGGTGC 50

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human glucagon gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GTGAGGCTAA ACAGAGCTGG AGAGTATATA AAAGCAGTGC GCCTTGGTGC A 51

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

AGGTGGAAAC ACTCTGCTGG TATAAAAGCA GGTGAGGACT TCATTAACTG 50

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human chorionic gonadotropin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

TTGAACTGTG GTGCAGGAAA GCCTCAAGTA GAGGAGGGTT GAGGCTTCAA 50

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human beta-LH gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GCCGCCCCCA CAACCCCGAG GTATAAAGCC AGATACACGA GGCAGGGGAT 50

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human follicle-stimulating hormone beta-subunit gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

TAGTTGCACA TGATTTTGTA TAAAAGGTGA ACTGAGATTT CATTCAGTCT 50

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human prolactin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

TATTCATGAA GATATCAAAG GTTTATAAAG CCAATATCTG GGAAAGAGAA 50

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human parathyroid gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GACATCATCT GTAACAATAA AAGAGCCTCT CTTGGTAAGC AGAAGACCTA 50

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Owl monkey insulin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

GGGGAGATGG GCTCTGGGCC TATAAAGCCA GCAGGGACCC AGCAGCCCTC 50

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: human insulin/IGF II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

CCCCGCCTCC AGAGTGGGGG CCAAGGCTGG GCAGGCGGGT GGACGGCCGG 50

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human insulin like growth factor
IGFII gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

AAAGAACTCT GCCTTGCGTT CCCCAAAATT TGGGCATTGT TCCGGCTCGC 50

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human insulin-like growth factor II gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

CCCTGGGCCG CGGCTGGCGC GACTATAAGA GCCGGGCGTG GGCGCCCGCA 50

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gastrin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

AGTTGGGAGG GACCTTGAGG GCTTTATAAG GCAGGCCTGG AGCATCAAGC 50

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon alpha gene INF-alpha 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GGAAATCAGT ATGTTCCCTA TTTAAGGCAT CTGCAGGAAG CAAAGCCTTC 50

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for leukocyte interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGAAGCTAGT ATGTTCCTTA TTTAAGACCT ATGCACAGAG CAAGGTCTTC 50

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon alpha gene
INF-alpha 4b

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GGAAATTAGT ATGTTCACTA TTTAAGACCT ATGCACAGAG CAAAGTCTTC 50

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for leukocyte (alpha) interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GGAAATTAGT ATGTTCACTA TTTAAGGCCT ATGCACAGAG CAAAGTCTTC 50

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon genes LeIF-L and LeIF-J

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GGAAATTAGT ATGTTCACTA TTTAAGACCT ATGCACAGAG CAAAGTCTTC 50

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human gene for fibroblast (beta-1) interferon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

ATAGAGAGAG GACCATCTCA TATAAATAGG CCATACCCAC GGAGAAAGGA 50

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human c-sis gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

CTCTCGCACT CTCCCTTCTC CTTTATAAAG GCCGGAACAG CTGAAAGGGT 50

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human migratory inhibitory factor-related protein 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

CAGCTGGCCA AGCCTAACCG CTATAAAAAG GAGCTGCCTC TCAGCCCTGC 50

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human migratory inhibitory factor-related protein 14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GTGCCCCAGT CAGGAGCTGC CTATAAATGC CGAGCCTGCA CAGCTCTGGC 50

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human epidermal growth factor related gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GGTCCCTCCT CCTCCCGCCC TGCCTCCCGC GCCTCGGCCC GCGCGAGCTA 50

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human opsin gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GCTTAGGAGG GGGAGGTCAC TTTATAAGGG TCTGGGGGGG TCAGAACCCA 50

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human blue cone photoreceptor pigment gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

TTTTGTGGGG TGGGAGGATC ACCTATAAGA GGACTCAGAG GAGGGTGTGG 50

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human red cone photoreceptor pigment gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

CGGGCTGATC CCACAGGCCA GTATAAAGCG CCGTGACCCT CAGGTGATGC 50

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human green cone photoreceptor pigment gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

CGGGCTGATC CCACTGGCCG GTATAAAGCG CCGTGACCCT CAGGTGACGC 50

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon-inducible gene IFI-56K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

TTGGCTGCTG TTTAGCTCCC TTATATAACA CTGTCTTGGG GTTTAAACGT 50

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human interferon-induced 15-Kd protein (ISG) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GACGTGTGTG CCTCAGGCTT AATAATAGGG CCGGTGCTGC TGCGGAAGCC 50

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human ubiquitin-like protein (GdX) gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

TCCAGCGCGC GCGCCCGGGG CGGCGGCGCG CGGCGGGGGG TGGTTGGGGT 50

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human exogenous retrovirus erv3 5" long terminal repeat

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

CCGCCCCTGT TGGTTGCATG TATAAAAGTC AAGCCCTGTC ATTGTTCAGG 50

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Bovine leukemia virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

ACCTCACCTG CTGATAAATT AATAAAATGC CGGCCCTGTC GAGTTAGCGG 50

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell lymphotropic virus type I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

TCAATAAACT AGCAGGAGTC TATAAAAGCG TGGAGACAGT TCAGGAGGGG 50

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell leukemia virus II proviral LTR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

TCAAAATAAA AGATGCCGAG TCTATAAAAG CGCAAGGACA GTTCAGGAGG 50

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human T-cell Lymphotropic virus type III (HIV-1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GGCGAGCCCT CAGATCCTGC ATATAAGCAG CTGCTTTTTG CCTGTACTGG 50

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Aids-associated retrovirus (arv-2;proviral)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

TGGCGTCCCT CAGATGCTGC ATATAAGCAG CTGCTTTTTG CCTGTACTGG 50

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human immunodeficiency virus type 2 (HIV-2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GCCCTCATAT TCTCTGTATA AATATACCCG CTAGCTTGCA TTGTACTTCG 50

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Visna lentivirus, Icelandic strains LV1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

CATAACCGCA GATGTAAACA AGTTGCCTAT ATAAGCCGCT TGCTAGCTGG 50

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Human cytomegalovirus strain AD169 gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GGCGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCGTTT AGTGAACCGT 50

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Murine cytomegalovirus intermediate-early gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GCTGAGCTGC GTTCACGTGG GTATAAGAGG CGCGACCAGC GTCGGTACCG 50

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus intermediate-early glycoprotein UL37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CGTCATGTCC GGCATCTTCA TGTATATAAG ACGGTGTTTC AAGACGACGT 50

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus I-E glycoprotein US3 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

ACAACGTCAC CAAGAAACGC TATATATTCA AAAACACCGT TCAGTCCACA 50

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes Simplex Virus type 1 gene I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

TTTGGGGAGG GGAAAGGCGT GGGGTATAAG TTAGCCCTGG CCCGACAGTC 50

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes Simplex Virus type 1 gene II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

AGCCGGCCCC GGCACCACGG GTATAAGGAC ATCCACCACC CGGCCGGTGG 50

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus type II I-E gene II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

AGCCGGCCCC GGTCGTGCGG GTATAAGGGC AGCCACCGGC CCACTGGGCG 50

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus type I I-E gene III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

TTCCCGCCGG CCCCTGGGAC TATATGAGCC CGAGGACGCC CCGATCGTCC 50

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus type II I-E gene III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

CCCCGCGCGC CCCGAGCGAC TATATCAGCC AGGCGACGGG GCGATCGTCC 50

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus type 1 I-E genes IV and V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

GGGGGCGGGT CTCTCCGGCG CACATAAAGG CCCGGCGCGA CCGACGCCCG 50

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus type 2 I-E genes IV and V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

ACGGGGGGCG GGCCGTTCCT CGCGCACATA AAGGGCCGGC GTCCCGGTCG 50

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus DNA polymersase gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

TAGGCGGGCT GGAAAGATGA TGTATAAATA GAGTCTGCGA CGGGGTTCGG 50

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus b' 2.2 kb transcript (start 160513)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

TAGGCGGGCT GGAAAGATGA TGTATAAATA GAGTCTGCGA CGGGGTTCGG 50

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus 2.7 kb transcript (start 4578)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GCCCGCGCTC GGCAGAGCTA CCATATAAAA ACGCAGGGGT TTAGCAGCTT 50

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 82K AlkExo (start 27048)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

CAGCACCAGG AGAGGCTTAA GCTCGGGAGG CAGCGCCACC GACGACAGTA 50

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 42K gene (start site 106547)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

ATGGGTTGTG GTTATATGCA CTTCCTATAA GACTCTCCCC CACCGCCCAC 50

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 39k dUTPase gene (start 106811)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

CGTGTGCGAT AATACACACG CCCATCGAGG CCATGCCTAC ATAAAAGGGC 50

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 33K (start site 145165)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGCCGGGCGA CCCAGATGTT TACTTAAAAG GCGTGCCGTC CGCCGGCATG 50

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 21K (start site 145459)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

CGACGTACGC GATGAGATCA ATAAAAGGGG GCGTGAGGAC CGGGAGGCGG 50

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' 5 kb transcript (start 86216)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CCCCACCCCT GCGCGATGTG GATAAAAAGC CAGCGCGGGT GGTTTAGGGT 50

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' RNR2 gene (start 89774)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GGTCCGCCTT CTGGTCCACG CATATAAGCG CGGACTAAAA ACAGGGATGT 50

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 RNR2 gene (start site 247)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

TGGTCCGCCT TCTCGTCCAC GCATATAAGC GCGGCCTGAA GACGGGGATG 50

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' tk gene (start site 47911)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

CGCGGTCCCA GGTCCACTTC GCATATTAAG GTGACGCGTG TGGCCTCGAA 50

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 b' tk gene (start site 225)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

CGCGGCCCGA GGTCCACTTC GCATATTAAG GTGACGCGCG TGGCCTCGAA 50

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' dbp gene (start site 62318)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

CGGCACGCCC CCAGGTAAAG TGTACATATA CCAACCGCAT ACCAGACGCA 50

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gB (3.3 Kb) start 56081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

CCACTCAGCG CGCCGCCTGG CGATATATTC GCGAGCTGAT TATCGCCACC 50

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gD (start 138337)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

CCACTCAGCG CGCCGCCTGG CGATATATTC GCGAGCTGAT TATCGCCACC 50

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 b' gD (start 5918)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GGAGTATAAT AGAGTCTTTG TGTTTAAAAC CCGGGGTCGG TGTGGTGTTC 50

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' gE (start site 141171)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GGAGAGGGCC CGCGGCGCAT TTAAGGCGTT GTTGTGTTGA CTTTGCCTCT 50

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 ICP gene (start site 58361)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

AATTATTGCT ACGACATCCG TGCTTGTTTG TGTTCCGTGT CTATATCTCT 50

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b' tr-4
(start site 136729)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GGCGGTGCTG TTTGCGGGTT GGCACAAAAA GACCCCGATC CGCGTCTGTG 50

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 [U-S] b' tr-9
(start 143245)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GTGACGTCAA TTGCCCGAGG CGCATAAAGG GCCGGTGGTC CGCCTAGCCG 50

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' VP5
(start 40768)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GGGGTGGGGC GGGGGGGGGG GTATATAAGG CCTGGGATCC CACGTCCCCG 50

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' 2.1kb transcript (start 26639)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

CCCGTTAACC CCCCACGTGA TCAGCACGCC ACCGACACCG CAGACGAAAA 50

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' a'TIF/VSP (start 105259)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GGGGCGGCCC GTGCGGGTTG CTTAAATGCG TGGTGGCGAC CACGGGCTGT 50

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 b'g' 2.7 kb transcript (start 100998)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GCCACGCCCA TAAGCTCCTC CCGATAAAAA GCGCCCCGAT GGCCCTGGAC 50

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus UL36 gene (start 49862)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GACGTCAACG CTGATAGTGT CTATAAAGGC CGTGCCGCCG CGCCGTAGTT 50

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp65 gene (start 121072)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

TCCGCGTTTG GTCGCCTGCC TATGTAAGGC GGCGGCCGCA GAGGGCGCGC 50

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp71 gene (start 119223)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GTCACCGCTG CTATATTTGC GACAGTTGCC GGAACCCTTC CCGACCTCCC 50

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human cytomegalovirus g' pp150 gene (start 43092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

CGTATCCGCC TCCGCTATTA AACTACCCCC CCTCCCTCTA GGTGGGGCGC 50

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' 5 Kb transcript (start 103313)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

TTGTGTCGCA GGGCGGCCCG CGTATAAAGG CGAGAGCGCG GGACCGTTTC 50

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' gC (start 96170)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

AACCCCGGAT GGGGCCCGGG TATAAATTCC GGAAGGGGAC ACGGGCTACC 50

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 g' gC (start 670)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GCGGGGGTGC CGTGGACGGG TATAAAGGCC AGGGGGGCAC GCGGGCCCAT 50

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' gH gene (start 46581)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

CGGCAATAAA AAGACAGAAT AAAACGCACG GGTGTTGGGT CGTTTGTTCA 50

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 g' 42 K (start site 107130)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

CCGGAGTCCC CGCTAACCTT CGGCATAAAA GCCACCGCGC GCCTGTTGAC 50

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 Ori_s ORF (start site 132287)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

CGGAGGCCCC CGGGGTGCGT CCCCTGTGTT TCGTGGGTGG GGTGGGCGGG 50

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-1 18 K (start site 97951)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

CCCGCCCACC GCTGGGCGCT ATAAAGCCGC CACCCTCTCT TCCCTCAGGT 50

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Herpes simplex virus-2 18K (start site 2391)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

CCCCGCCGTC CCCCGGGCGT TATAAGCCGC CGCACTCGCT TTTCCCACCG 50

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus L1 1Kb gene (start site 103194)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

TGGTGCCTTG GCTTTAAAGG GGAGATGTTA GACAGGTAAC TCACTAAACA 50

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 145K gene (start site 1721)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

ACTGTATAAA GGTAAGTATT ATTAAATTTT AGAGACACTA TCACGTGTAA 50

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 20K (start site 9660)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

CTTTTAGCCA TGCCATGCTC TATAAATCAC TTCCCTATCT CAGGTAGGCC 50

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [DL/R] (start site 52787)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

ACAGAGACCC CAAAAAGAGG ATAAAAGAAG GCGAGCCGGC CCGGCTCGCC 50

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R2 (start site 61372)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GTGACGGTCA GGCAGCTCCT GTATTTAACT TTGCGGACAG AGGCCAGAGC 50

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus L2 (start site 57050)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

TAATTACGCT TGTGTACATA TTTAAATCCA CACAAGTGGC CAGAGTGGGC 50

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R1 (start site 88539)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GACAGGGACG GCGGCGCTAT ATATAAGAGC CCAAGACCCG GCTCTCTTTA 50

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus R2 (start site 88897)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

CGGATTAGAT GGGGATATTT AAAAGGGGCA GCAATCTCGG CTGTTTGTAC 50

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus L2 (start site 90021)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

ACCCAACAGG TGGTGAAAAT ATAACACAGG TGACACCAGC CTCTATCAGC 50

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-L] L1 (start site 92157)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

ACCCCCCTTG TACCTATTAA AGAGGATGCT GCCTAGAAAT CGGTGCCGAG 50

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-L] L3
(start site 88480)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

CGGGTCTTGG GCTCTTATAT ATAGCGCCGC CGTCCCTGTC TGTTAGATCA 50

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-K] 2.1 Kb
(start site 109939)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

AGACGCCCTC AATCGTATTA AAAGCCGTGT ATTCCCCCGC ACTAAAGAAT 50

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-K] 1.3kb transcript (start 110632)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

TTGCGACCCC TCTGATATTA AGGTGGTTAT TTTGGGCCAG GACCCCTATC 50

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-H] L1 (start site 137680)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

CGGTGCCCGG ACTCAGAATT ATTAAACCGG GTGGCAGCTC CTGGCAGTCA 50

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L1 (start site 159337)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

AAGGGCAGGG GGTGGGTATT TAAGGATCTA TATGCCCTTC TCTACCTGCA 50

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] R1
(start 165496)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

AATGGGCGTG GCAGAATAGT ATAAGACGCG AGGCCTGGGT GAGGAGAGTC 50

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L2
(start 167495)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

TCTTTCCTTG TCCTTACTGT ATAAAAGTCC ACGAAAACAG CTGTGCCTCA 50

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr Virus [EcoR1-D] L1A
start 169165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

ACTGATGAGT AAGTATTACA CCCTTTGCCC CACACCCCCT TTCCCTTACT 50

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr Virus [EBNA] E1 (start site 11333)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

AGGGGGGGAC TAAGGTCCCA CTACAAAAAC TCTGTGTTCT GCTGCAAATT 50

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EBNA] E2 (start site 14399)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GGTATAAAGT GGTCCTGCAG CTATTTCTGG TCGCATCAGA GCGCCAGGAG 50

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [EcoR1-D] L1 (start site 169514)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

CTCTGACGTA GCCGCCCTAC ATAAGCCTCT CACACTGCTC TGCCCCCTTC 50

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type 2 EIa (start 498)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GTCAGCTGAC GCGCAGTGTA TTTATACCCG GTGAGTTCCT CAAGAGGCCA 50

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-5 EIa (start 499)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GTCAGCTGAC GTGTAGTGTA TTTATACCCG GTGAGTTCCT CAAGAGGCCA 50

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-7 EIa (start site 512)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TCAGCTGATC GCTAGGGTAT TTAAACCTGA CGAGTTCCGT CAAGAGGCCA 50

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-12 Ela (start site 306)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

AAATTGATGA CGGCAATTTT ATTATAGGCG CGGAATATTT ACCGAGGGCA 50

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-12 EIa (start site 445)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GTCAGCTGAT CGTTTGGGTA TTTAATGCCG CCGTGTTCGT CAAGAGGCCA 50

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Simian Adenovirus SA7 EIa (start site 440)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

TTATTGTCTA GGTGAGGGTA TTTAAACCGG CTCAGACCGT CAAGAGGCCA 50

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 EIb (start 1700)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GGGGCGGGGC TTAAAGGGTA TATAATGCGC CGTGGGCTAA TCTTGGTTAC 50

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-5 EIb (start site 1703)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GGGGCGGGGC TTAAAGGGTA TATAATGCGC CGTGGGCTAA TCTTGGTTAC 50

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-7 EIb (start site 1577)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

TTCTTGGGTG GGGTCTTGGA TATATAAGTA GGAGCAGATC TGTGTGGTTA 50

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-12 EIb (start site 1527)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TGGGCGTGGT TAAACAGGGA TATAAAGCTG GGTTGGTGTT GCTTTGAATA 50

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 EII (start site 27092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAAAGGGCGC GAAACTAGTC CTTAAGAGTC AGCGCGCAGT ATTTGCTGAA 50

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 EIII (start site 27610)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TGCGGTCGCC CGGGCAGGGT ATAACTCACC TGAAAATCAG AGGGCGAGGT 50

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-5 EIII (start site 239)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

TGCGGTCGCC CGGGCAGGGT ATAACTCACC TGACTCTTGG AGGGCGAGGT 50

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 EIV (start site 35611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

TTACGTCATT TTTTAGTCCT ATATATACTC GCTCTGTACT TGGCCCTTTT 50

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 IVa2 (start site 5827)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

CCCTCCCACT TAGCCTCCTT CGTGCTGGCC TGGACGCGAG CCTTCGTCTC 50

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-5 IVa2 (start site 5837)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

CCCTCCCACT TAGCCTCCTT CGTGCTGGCC TGGACGCGAG CCTTTGTCTC 50

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-7 IVa2 (start site 5692)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

CCCTCCCACG TGGCCTCCTT TGTGCTGGCC TGGACACGCG CTTTTGTATC 50

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 IX (start site 3575)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GCTTAAGGGT GGGAAAGAAT ATATAAGGTG GGGGTCTCAT GTAGTTTTGT 50

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-5 IX (start site 3581)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GCTTAAGGGT GGGAAAGAAT ATATAAGGTG GGGGTCTTAT GTAGTTTTGT 50

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-7 IX (start site 3460)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

ATGGGGACTT TCAGGTTGGT AAGGTGGACA AATTGGGTAA ATTTTGTTAA 50

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 major late (start site 6039)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GTGTTCCTGA AGGGGGGCTA TAAAAGGGGG TGGGGGCGCG TTCGTCCTCA 50

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-5 major late (start site 6049)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GTGTTCCTGA AGGGGGGCTA TAAAAGGGGG TGGGGGCGCG TTCGTCCTCA 50

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-7 major late (start site 5904)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GGGTCCCCGC CGGGGGGGTA TAAAAGGGGG CGGACCTCTG TTCGTCCTCA 50

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-12 major late (start site 972)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

AATTTTCTGG TGGTGGGCTA TAAAAAGGGG CGGGTCCTTG GTCTTCATCG 50

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Adenovirus type-2 LIIa (start site 25954)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GGCGTGGTAG TCCTCAGGTA CAAATTTGCG AAGGTAAGCC GACGTCCACA 50

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human papilloma virus type 18 E6 gene (start site 30)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

CAGCACATAC TATACTTTTC ATTAATACTT TTAACAATTG TAGTATATAA 50

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human papilloma virus type-16 E6/E7 (start site 97)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAACCGAAAC CGGTTAGTAT AAAAGCAGAC ATTTTATGCA CCAAAAGAGA 50

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human papilloma virus type-18 E6 (start site 105)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GGACCGAAAA CGGTGTATAT AAAAGATGTG AGAAACACAC CACAATACTA 50

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Parvovirus h-1 H-1[+.04] (start site 209)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

AGTGGGCGTG GCTAACTGTA TATAAGCAGT CACTCTGGTC GGTTACTCAC 50

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Parvovirus h-1 H-1 [+.40] (start site 2010)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GCCGAAGCTA GACACTCCTA TAAATTCGCT AGGTTCAATG CGCTCACCAT 50

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Human parvovirus B19-Au B19 [0.06] (start site 347)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAGCGTAGGC GGGGACTACA GTATATATAG CACGGTACTG CCGCAGCTCT 50

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start site 31)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

CCGCCCCTAA CTCCGCCCAG TTCCGCCCAT TCTCCGCCCC ATGGCTGACT 50

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Simian virus 40 T/t early P2 (start site 5233)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCCT 50

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: BK virus T/t early (start site 99)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

CCTGTGGCCT TTTTTTTTAT AATATATAAG AGGCCGAGGC CGCCTCTGCC 50

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Polyoma virus T/t E (start site 156)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

GGCCACCCAA ATTGATATAA TTAAGCCCCA ACCGCCTCTT CCCGCCTCAT 50

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Simian virus 40 late (start site 325)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

GTTCTTTCCG CCTCAGAAGG TACCTAACCA AGTTCCTCTT TCAGAGGTTA 50

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 3.6kb P1 (start 1659)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

AGTTGGGGGA GGAGATTAGG TTAAAGGTCT TTGTACTAGG AGGCTGTAGG 50

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Heptitis B virus subtype adr4 3.6 kb P2 (start 1690)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

TGTACTAGGA GGCTGTAGGC ATAAATTGGT CTGTTCACCA GCACCATGCA 50

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 2.2 kb P1 (start 3061)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

ATCGGCAGTC AGGAAGACAG CCTACTCCCA TCTCTCCACC TCTAAGAGAC 50

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Hepatitis B virus subtype adr4 2.2 kb P2 (start 3092)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

CTCTCCACCT CTAAGAGACA GTCATCCTCA GGCCATGCAG TGGAACTCCA 50

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Epstein Barr virus [BamH1-F] R1 (start 58862)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

TATTTTTGAA AAGGGATATT ATAAAACAGG TCATTGCTCG GATTGTGGCA 50

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Promoter Sequence of IL-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GGTGTGAGGC GTCACCACTT GGGCCTATAA AAGCTGCCAC AAGACGCCAA GGCCAC 56

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oriS, higher affinity

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

CGTTCGCACT T 11

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oriS, lower affinity

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

TGCTCGCACT T 11

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9Z1 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GCGCGCGCGC GTTCGCACTT CCGCCGCCGG 30

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9Z2 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GGCGCCGGCC GTTCGCACTT CGCGCGCGCG 30

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 CCCG TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GGCCCGCCCC GTTCGCACTT CCCGCCCCGG 30

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 GGGC TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GGCGGGCGCC GTTCGCACTT GGGCGGGCGG 30

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 ATAT TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GGATATATAC GTTCGCACTT TAATTATTGG 30

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 polyA TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GGAAAAAAAC GTTCGCACTT AAAAAAAAGG 30

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 polyT TEST SEQ. / UL9 ASSAY

SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GGTTTTTTTC GTTCGCACTT TTTTTTTGG 30

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 GCAC TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GGACGCACGC GTTCGCACTT GCAGCAGCGG 30

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 ATori-1 Test sequence / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GCGTATATAT CGTTCGCACT TCGTCCCAAT 30

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: oriECO2 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GGCGAATTCG ACGTTCGCAC TTCGTCCCAA T 31

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: oriECO3 TEST SEQ. / UL9 ASSAY SEQ.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GGCGAATTCG ATCGTTCGCA CTTCGTCCCA AT 32

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: WILD TYPE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

AAGTGAGAAT TCGAAGCGTT CGCACTTCGT CCCAAT 36

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: TRUNCATED UL9 BINDING SITE, COMPARE SEQ ID NO:601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

TTCGCACTT 9

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: HSVB1/4, SEQUENCE OF COMPETITOR DNA MOLECULE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GGTCGTTCGC ACTTCGC 17

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 14B, top strand of an exemplary target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GCGTANNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT 37

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: HSV primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

ATTGGGACGA AG 12

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: a sample distamycin target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

TTCCTCCTTT C 11

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: a distamycin target sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

TTCCNNNTTT C 11

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 27A, test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GCGTANNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT 37

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 27B, oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

GCGTANNNNN CGTTCGCACT TNNNNCTTCG TCCCAAT 37

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 27C, oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GCGTANNNNN AAGTGCGAAC GNNNNCTTCG TCCCAAT 37

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 27D, oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GCGTANNNNN AAGTGCGAAC GNNNNCTTCG TCCCAAT 37

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: -35 region consensus sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

TTGACA 6

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: -10 region consensus sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

TATAAT 6

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: HIV-1, LTR sequence, Figure 28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GTTAGAGTGG AGGTTTGACA GCCGCCTAGC ATTTCATCAC ATGGCCCGAG AGCTGCATCC 60

GGAGTACTTC AAGAACTGCT GACATCGAGC TTGCTACAAG GGACTTTCCG CTGGGGACTT 120

TCCAGGGAGG CGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT CCTGCATATA 180

AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA GCCTGGGAGC 240

TC 242

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: a TFIID binding site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

CCTGCATA 8

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: a TFIID binding site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AAGCAGCT 8

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GCAGAATTCT GCAG 14

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GCAGAATTCT GCAGCGTTCG CACTTTCTAG AGCTCAGG 38

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

AGATCTCGAG TCC 13

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GCAGAATTCT GCAGNNNNCG TTCGCACTTT CTAGAGCTCA GG 42

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GCAGAATTCT GCAGNNNNNN NNCGTTCGCA CTTTCTAGAG CTCAGG 46

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 29D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GCAGAATTCT GCAGCGTTCG CACTTNNNNN NNNTCTAGAG CTCAGG 46

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

CGTGAATTCT GCAG 14

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

CGTGAATTCT GCAGATG 17

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

CGTGAATTCT GCAGATGAGG TACCNNNNNN CGTTCGCACT TTCTAGAGCT CTCC 54

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GTGAAAGATC TCGAGAGG 18

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Oligonucleotide, Figure 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

AAGATCTCGA GAGG 14

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: UL9 BINDING SITE, HSV oriS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

CGTTCTCACT T 11

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Trimeric test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

ACGTACGTAC GT 12

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

AGCTTTCGCA CTTAGCT 17

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

AGCATTCGCA CTTAGCA 17

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

AGCCTTCGCA CTTAGCC 17

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

AGCGTTCGCA CTTAGCG 17

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

TGCTTTCGCA CTTTGCT 17

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

TGCATTCGCA CTTTGCA 17

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

TGCCTTCGCA CTTTGCC 17

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

TGCGTTCGCA CTTTGCG 17

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

CCATTTCGCA CTTCCAT 17

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

CCCTTTCGCA CTTCCCT 17

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

CCGTTTCGCA CTTCCGT 17

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 12 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CCTTTTCGCA CTTCCTT 17

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

TTCCNTTCC 9

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

TTCCNNTTCC 10

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

TTCCNNNTTC C 11

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 26 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

TTCCNNNNTT CC 12

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 31 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

CGTTCGCACT TTTAC 15

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 32 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

CCCGGGTACN 10

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Figure 32 test oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

CCCGGGACNN 10

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